GENOMIC SEQUENCES UPSTREAM OF THE CODING REGION OF THE IFN-ALPHA2 GENE FOR PROTEIN PRODUCTION AND DELIVERY

Field of the Invention

This invention relates to genomic DNA.

Background of the Invention

Current approaches to treating disease with therapeutic proteins include both administration of proteins produced *in vitro* and gene therapy. *In vitro* production of a protein generally involves the introduction of exogenous DNA coding for the protein of interest into appropriate host cells in culture. Gene therapy methods, on the other hand, involve administering to a patient cells, plasmids, or viruses that contain a sequence encoding the therapeutic protein of interest.

Certain therapeutic proteins may also be produced by altering the expression of their endogenous genes in a desired manner with gene targeting techniques. See, e.g., U.S. Patent Nos. 5,641,670, 5,733,761, and 5,272,071, U.S. Patent Application Serial No. 08/406,030, WO 91/06666, WO 91/06667, and WO 90/11354, all of which are incorporated by reference in their entirety.

Summary of the Invention

The present invention is based upon the identification and sequencing of genomic DNA 5' to the coding sequence of the human interferon-α 2 ("IFNA2") gene. This DNA can be used, for example, in a DNA construct that alters (e.g., increases) expression of an endogenous IFNA2 gene in a mammalian cell upon integration into the genome of the cell via homologous recombination. "Endogenous IFNA2 gene" refers to a genomic (i.e., chromosomal) gene that encodes IFNA2. The construct contains a targeting sequence including or

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derived from the newly disclosed 5' noncoding sequence, and a transcriptional regulatory sequence. The transcriptional regulatory sequence preferably differs in sequence from the transcriptional regulatory sequence of the endogenous IFNA2 gene. The targeting sequence directs the integration of the regulatory sequence into a region upstream of the endogenous IFNA2-coding sequence such that the regulatory sequence becomes operatively linked to the endogenous coding sequence. By "operatively linked" is meant that the regulatory sequence can direct expression of the endogenous IFNA2-coding sequence. The construct may additionally contain a selectable marker gene to facilitate selection of cells that have stably integrated the construct, and/or another coding sequence linked to a promoter.

In one embodiment, the DNA construct comprises: (a) a targeting sequence, (b) a regulatory sequence, (c) an exon, (d) a splice-donor site, (e) an intron, and (f) a splice-acceptor site, wherein the targeting sequence directs the integration of itself and elements (b) - (f) such that elements (b) - (f) are within or upstream of the endogenous gene. The regulatory sequence then directs production of a transcript that includes not only elements (c) - (f), but also the endogenous IFNA2 coding sequence. Preferably, the intron and the splice-acceptor site are situated in the construct downstream from the splice-donor site.

The targeting sequence is homologous to a pre-selected target site in the genome with which homologous recombination is to occur. It contains at least 20 (e.g., at least 30, 50, 100, or 1000) contiguous nucleotides of SEQ ID NO:12; and can contain, for instance, at least 20 (e.g., at least 30, 50, or 100) contiguous nucleotides of SEQ ID NO:7, at least 20 (e.g., at least 30 or 50) contiguous nucleotides of SEQ ID NO:8,

or at least 20 (e.g., at least 30, 50, 100, or 1000) contiguous nucleotides of SEQ ID NO:13. In addition, the targeting sequence can contain at least 20 (e.g., at least 30, 50, or 100) contiguous nucleotides of SEQ ID NO:16, at least 20 contiguous nucleotides of SEQ ID NO:17, at least 20 (e.g., at least 30 or 50) contiguous nucleotides of SEQ ID NO:18, or at least 20 (e.g., at least 30, 50, 100, or 1000) contiguous nucleotides of SEQ ID NO:19. SEQ ID NO:7 corresponds to nucleotides 1 to 278 of SEQ ID NO:12; SEQ ID NO:8 corresponds to nucleotides 3492 to 3564 of SEQ ID NO:12; and SEQ ID NO:13 corresponds to nucleotides 279 to 3491 of SEQ ID NO:12. By "homologous" is meant that the targeting sequence is identical or sufficiently similar to its genomic target site so that the targeting sequence and target site can undergo homologous recombination within a human cell. A small percentage of basepair mismatches is acceptable, as long as homologous recombination can occur at a useful frequency. To facilitate homologous recombination, the targeting sequence is preferably at least about 20 (e.g., at least 50, 100, 250, 400, or 1,000) base pairs ("bp") long. The targeting sequence can also include genomic sequences from outside the region covered by SEQ ID NO:12, so long as it includes as least 20 nucleotides from within this region. For example, additional targeting sequence could be derived from the sequence lying between SEQ ID NO:8 and the endogenous transcription initiation sequence of the IFNA2 gene.

Due to polymorphism that exists at the IFNA2 genetic locus, minor variations in the nucleotide composition of any given genomic target site may occur in any given mammalian species. Targeting sequences that correspond to such polymorphic variants of SEQ ID NOs:7, 8, 12, 13, 16, 17, 18, and 19 (particularly human

polymorphic variants) are within the scope of this invention.

Upon homologous recombination, the regulatory sequence of the construct is integrated into a pre-selected region upstream of the coding sequence of an IFNA2 gene in a chromosome of a cell. The resulting new transcription unit containing the construct-derived regulatory sequence alters the expression of the target IFNA2 gene. The IFNA2 protein so produced may be identical in sequence to the IFNA2 protein encoded by the unaltered, endogenous gene, or may contain additional, substituted, or fewer amino acid residues as compared to the wild type IFNA2 protein, due to changes introduced as a result of homologous recombination.

Altering gene expression encompasses activating (or causing to be expressed) a gene which is normally silent (i.e, essentially unexpressed) in the cell as obtained, increasing or decreasing the expression level of a gene, and changing the regulation pattern of a gene such that the pattern is different from that in the cell as obtained. "Cell as obtained" refers to the cell prior to homologous recombination.

Also within the scope of the invention is a method of using the present DNA construct to alter expression of an endogenous IFNA2 gene in a mammalian cell. This method includes the steps of (i) introducing the DNA construct into the mammalian cell, (ii) maintaining the cell under conditions that permit homologous recombination to occur between the construct and a genomic target site homologous to the targeting sequence, to produce a homologously recombinant cell; and (iii) maintaining the homologously recombinant cell under conditions that permit expression of the IFNA2 coding sequence under the control of the construct-derived regulatory sequence. At least a part of the genomic

target site is 5' to the coding sequence of an endogenous IFNA2 gene. That is, the genomic target site can contain coding sequence as well as 5' non-coding sequence.

The invention also features transfected or infected cells in which the construct has undergone homologous recombination with genomic DNA upstream of the endogenous ATG initiation codon in one or both alleles of the endogenous IFNA2 gene. Such transfected or infected cells, also called homologously recombinant cells, have an altered IFNA2 expression pattern. These cells are particularly useful for *in vitro* IFNA2 production and for delivering IFNA2 via gene therapy. Methods of making and using such cells are also embraced by the invention. The cells can be of vertebrate origin such as mammalian (e.g., human, non-human primate, cow, pig, horse, goat, sheep, cat, dog, rabbit, mouse, guinea pig, hamster, or rat) origin.

The invention further relates to a method of producing a mammalian IFNA2 protein *in vitro* or *in vivo* by introducing the above-described construct into the genome of a host cell via homologous recombination. The homologously recombinant cell is then maintained under conditions that allow transcription, translation, and optionally, secretion of the IFNA2 protein.

The invention also features isolated nucleic acids comprising a sequence of at least 20 (e.g., at least 30, 50, 100, 200, or 1000) contiguous nucleotides of SEQ ID NO:12 or its complement, or of a sequence identical to SEQ ID NO:12 except for polymorphic variations or other minor variations (e.g., less than 5% of the sequence) which do not prevent homologous recombination with the target sequence. For instance, the isolated DNA can contain at least 20 (e.g., at least 30, 50, or 100) contiguous nucleotides of SEQ ID NO:7 or its complement, at least 20 (e.g., at least 30 or 50) contiguous

nucleotides of SEQ ID NO:8 or its complement, at least 20 (e.g., at least 30, 50, 100, or 1000) contiguous nucleotides of SEQ ID NO:13 or its complement, at least 20 (e.g., at least 30, 50, or 100) contiguous nucleotides of SEQ ID NO:16 or its complement, at least 20 contiguous nucleotides of SEQ ID NO:17 or its complement, at least 20 (e.g., at least 30 or 50) contiguous nucleotides of SEQ ID NO:18 or its complement, or at least 20 (e.g., at least 30, 50, 100, or 1000) contiguous nucleotides of SEQ ID NO:19 or its complement.

In one embodiment, the isolated nucleic acid of the invention includes a contiguous 100 bp block of SEQ ID NO:12. For example, the isolated DNA can contain nucleotides 1 to 100, 101 to 200, 201 to 300, 301 to 400, 401 to 500, 501 to 600, 601 to 700, 701 to 800, 801 to 900, 901 to 1000, 1001 to 1100, 1101 to 1200, 1201 to 1300, 1301 to 1400, 1401 to 1500, 1501 to 1600, 1601 to 1700, 1701 to 1800, 1801 to 1900, 1901 to 2000, 2001 to 2100, 2101 to 2200, 2201 to 2300, 2301 to 2400, 2401 to 2500, 2501 to 2600, 2601 to 2700, 2701 to 2800, 2801 to 2900, 2901 to 3000, 3001 to 3100, 3101 to 3200, 3201 to 3300, 3301 to 3400, 3401 to 3500, or 3465 to 3564 of SEQ ID NO:12 or its complement. These blocks of SEQ ID NO:12 or its complement are also useful as targeting sequences in the constructs of the invention.

In the isolated DNA, the SEQ ID NO:12-derived sequence is not linked to a sequence encoding intact IFNA2, or at least is not linked in the same configuration (i.e., separated by the same noncoding sequence) as occurs in any wild-type genome. The term "isolated DNA", as used herein, thus does not denote a chromosome or a large piece of genomic DNA (as might be incorporated into a cosmid or yeast artificial chromosome) that includes not only part or all of SEQ ID NO:12, but also an intact IFNA2-coding sequence and all

of the sequence which lies between the IFNA2 coding sequence and the sequence corresponding to SEQ ID NO:12 as it exists in the genome of a cell. It does include, but is not limited to, a DNA (i) which is incorporated into a plasmid or virus; or (ii) which exists as a separate molecule independent of other sequences, e.g., a fragment produced by polymerase chain reaction ("PCR") or restriction endonuclease treatment. The isolated DNA preferably does not contain a sequence which encodes intact IFNA2 precursor (i.e., IFNA2 complete with its endogenous secretion signal peptide).

The invention also includes isolated DNA comprising a strand which contains a sequence that is at least 100 (e.g., at least 200, 400, or 1000) nucleotides in length and that hybridizes under either moderately stringent or highly stringent conditions with SEQ ID NO:7, 8, 12, 13, 16, 17, 18, and/or 19, or the complement of SEQ ID NO:7, 8, 12, 13, 16, 17, 18, and/or 19. The sequence is not linked to an IFNA2-coding sequence, or at least is not linked in the same configuration as occurs in any wild-type genome. By moderately stringent conditions is meant hybridization at 50°C in Church buffer (7% SDS, 0.5% $NaHPO_4$, 1 M EDTA, 1% bovine serum albumin) and washing at 50°C in 2X SSC. Highly stringent conditions are defined as: hybridization at 42°C in the presence of 50% formamide; a first wash at 65°C with 2X SSC containing 1% SDS; followed by a second wash at 65°C with 0.1X SSC.

Also embraced by the invention is isolated DNA comprising a strand which contains a sequence that (1) is at least 50 (e.g., at least 70 or 100) nucleotides in length and (2) shares at least 80% (e.g., at least 85%, 90%, 95%, or 98%) sequence identity with a fragment or all of SEQ ID NO:12, or with the complement of the fragment. This fragment can include, for instance, a

part or all of SEQ ID NO:7, 8, 13, 16, 17, 18, or 19. The sequence is not linked to an intact IFNA2-coding sequence, or at least is not linked in the same configuration as occurs in any wild-type genome.

Where a particular polypeptide or nucleic acid molecule is said to have a specific percent identity or conservation to a reference polypeptide or nucleic acid molecule, the percent identity or conservation is determined by the algorithm of Myers and Miller, CABIOS (1989), which is embodied in the ALIGN program (version 2.0), or its equivalent, using a gap length penalty of 12 and a gap penalty of 4 where such parameters are required. All other parameters are set to their default positions. Access to ALIGN is readily available. See, e.g., http://www2.igh.cnrs.fr/bin/align-guess.cgi on the Internet.

The invention also features a method of delivering IFNA2 to an animal (e.g., a mammal such as a human, non-human primate, cow, pig, horse, goat, sheep, cat, dog, rabbit, mouse, guinea pig, hamster, or rat) by providing a cell whose endogenous IFNA2 gene has been activated as described herein, and implanting the cell in the animal, where the cell secretes IFNA2. Also included in the invention is a method of producing IFNA2 by providing a cell whose endogenous IFNA2 gene has been activated as described herein, and culturing the cell *in vitro* under conditions which permit the cell to express and secrete IFNA2.

The invention further includes isolated DNA that shares at least 80% (e.g., at least 85%, 90%, or 95%) sequence identity, or hybridizes under highly or moderately stringent conditions, with a portion (e.g., at least about 20, 50, 100, 400, or 1000 bp in length) of the HindIII-BamHI insert of plasmid pA2HB (described below). The 3' end of this portion of the insert is at

least 511 bp upstream of the ATG translation initiation codon of the IFNA2-coding sequence included in the plasmid insert.

The isolated DNA of the invention can be used, for example, as a source of an upstream PCR primer for use (when combined with a suitable downstream primer) in obtaining the regulatory region and/or complete coding sequence of an endogenous IFNA2 gene, or as a hybridization probe for indicating the presence of chromosome 9 in a preparation of human chromosomes. It can also be used, as described below, in a method for altering the expression of an endogenous IFNA2 gene in a vertebrate cell.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Exemplary methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. The materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

Brief Description of the Drawings

Fig. 1 is a representation of the published sequence (SEQ ID NO:1) of a human IFNA2-coding sequence and some flanking 5′ and 3′ non-coding sequences (GenBank

HUMIFNAA). Sequences of PCR primers IFN1, IFN2, IFN6, and IFN7 are indicated by arrows.

Fig. 2 is a schematic diagram showing the human IFNA2 genomic region encompassed by the insert of plasmid pA2HB.

Fig. 3 is a representation of the nucleotide sequence (SEQ ID NO:7) of a region upstream of the coding sequence of a human IFNA2 gene. This nucleotide sequence has not been reported previously.

Fig. 4 is a representation of a sequence (SEQ ID NO:9) of a human IFNA2-coding sequence and some flanking 5' and 3' non-coding sequences. The underlined sequence (SEQ ID NO:8) has not been previously reported. The polypeptide sequence (SEQ ID NO:2) encoded by this gene is also shown. The N-terminus of the mature polypeptide is indicated by "Mature."

Fig. 5 is a schematic diagram showing a construct of the invention. The construct contains a first targeting sequence (1); an amplifiable marker gene (AM); a selectable marker gene (SM); a regulatory sequence; a CAP site; an exon; a splice-donor site (SD); an intron; a splice-acceptor site (SA); and a second targeting sequence (2). The black boxes represent coding DNA and the stippled boxes represent transcribed but untranslated sequences.

Fig. 6 is a representation of a sequence (SEQ ID NO:11) of a human genomic sequence 5' to the IFNA2 coding sequence, and including some coding sequence. The underlined sequence is previously reported while the remainder (-4074 to -511; SEQ ID NO: 12) is new. The framed sequence is SEQ ID NO:13. The sequence 5' to SEQ ID NO:13 is SEQ ID NO:7. The sequence between the framed area and the underlined sequence is SEQ ID NO:8. Nucleotides -4074 to -3270 is SEQ ID NO:16. Nucleotides -3269 to -3239 is SEQ ID NO:17. Nucleotides -3241 to -

3137 is SEQ ID NO:18. Nucleotides -3139 to -511 is SEQ ID NO:19.

Fig. 7 is a representation of a first targeting sequence (SEQ ID NO: 14) used in a construct of the invention.

Fig. 8 is a representation of a second targeting sequence (SEQ ID NO: 15) used in a construct of the invention.

Detailed Description

The present invention is based on the discovery of the nucleotide composition of sequences upstream to the coding sequence of a human IFNA2 gene.

Interferon-α constitutes a complex gene family with 14 genes clustered on the short arm of chromosome 9. None of these genes, including the IFNA2 gene, have introns. Interferon-α is produced by macrophages, T and B cells, and a variety of many other cells. Interferon-α has considerable antiviral effects, and has been shown to be efficacious in treating infections by papilloma virus, hepatitis B and C viruses, vaccinia, herpes simplex virus, herpes zoster varicellosus virus, and rhinovirus.

The human IFNA2 gene encodes a 188 amino acid precursor protein (SEQ ID NO:2) containing a 23 amino acid signal peptide. The genomic map of the human IFNA2 gene is shown in Fig. 1. The map is constructed based on 1,733 base pair ("bp") published sequences (HUMIFNAA, GenBank accession number J00207 and V00544; SEQ ID NO:1) which begin at position -510 relative to the translational start site (unless otherwise specified, all positions referred to herein are relative to the translational start site), and end at position +1,223. The cap site is located at position -67.

Specific Sequences 5' to an IFNA2 Gene and Their Use in Altering Endogenous IFNA2 Gene Expression

To obtain genomic DNA containing sequence upstream to an IFNA2 gene, a human leukocyte genomic library in lambda EMBL3 (Clontech catalog # HL1006d) was screened with a 332 bp probe generated by PCR. This probe corresponds to the genomic region between positions -263 and +69, and was amplified from human genomic DNA using oligonucleotide primers designated IFN7 and IFN6, both of which were designed from the available IFNA2 genomic DNA sequence (Fig. 1). The 5' end of primer IFN7 corresponds to position -263, and the primer's sequence is 5'-AGTTTCTAAAAAGGCTCTGGGGTA-3' (SEQ ID NO:3). The 5' end of primer IFN6 corresponds to position +69, and this primer sequence is 5'-GCCCACAGAGCAGCTTGAC-3' (SEQ ID NO:4).

Approximately one million recombinant phage were screened with the radiolabelled 332 bp probe. Sixty positive plaques were isolated from the primary screening plates. Lambda phage DNA was isolated from thirty of these plaques and subjected to PCR assay using oligonucleotide primers IFN1 and IFN2. Both IFN1 and IFN2 are derived from the 3' untranslated region of the IFNA2 gene; their sequences can be found at the website "http://www.ncbi.nlm.nih.gov/dbSTS," using the identification code "NCBI_ID:42433." The 5' end of primer IFN1 corresponds to position +639, and the primer's sequence is 5'-AAAGACTCATGTTTCTGCTATGACC-3' (SEQ ID NO:5). The 5' end of primer IFN2 corresponds to position +853, and the primer's sequence is 5'-GGTGCACATGACATAATATGAACA-3' (SEQ ID NO:6). Of the thirty phage samples, two generated the expected 215 bp PCR product. One of the two phage plaques was further purified by two additional rounds of hybridization screening, yielding phage clone 4-4-1.

A 8.3 kb HindIII-BamHI fragment from phage 4-4-1 was subcloned into pBluescript II SK+ (Stratagene, La Jolla, CA) to produce pA2HB, which contains approximately 4.3 kb of untranscribed upstream sequences, the protein-coding region (1.1 kb), and approximately 2.8 kb of downstream sequences of the IFNA2 gene. A restriction map of the 8.3 kb HindIII-BamHI fragment is shown in Fig. 2.

The pA2HB plasmid was sequenced by the Sanger method. A 278 bp sequence whose 5' terminus is at the 5' end HindIII site is shown below (see also Fig. 3):

AAGCTTTTATAGGTGTAAATTTTCCACTTAGTACTGCTTTTG
TAATGTTGTCTTTTTATTTTCATTTATCTCAAGATGTTTTCT
AATTTCTCTTGACTTCCTTCTTAAATTCTTACCTCATGTAGA
CATACATTTTTGGCCCTATGCATTGGGATGCAAAACCAGACT
AATTTACTTTGTACAAAAAGAAAAATGAGAAAGAAATATATT
TGGTCTTGTGAGCACTATATGGAAATACTTTATATTCCATTT
GTTTCATCATATTCATATATCCCTTT (SEQ ID NO:7)

The HindIII site is located at position -4,073. A previously unpublished sequence between positions -583 and -511 was also determined, as shown below and as underlined in Fig. 4.

CATTGGATACTCCATCACCTGCTGTGATATTATGAATGTCTG
CCTATATAAATATTCACTATTCCATAACACA (SEQ ID NO:8)

The sequence (SEQ ID NO:13) between the regions corresponding to SEQ ID NOs:7 and 8 was also determined.

The genomic sequence between positions -4,074 and -511 (SEQ ID NO:12) is the sequence which is not underlined in Fig. 6. SEQ ID NOs:7 and 8 correspond to nucleotides 1-278 and nucleotides 3492-3564 of SEQ ID NO:12, respectively.

To alter the expression of an endogenous INFA2 gene, a DNA fragment containing nucleotides 279-3311 of SEQ ID NO:12 was cloned into a plasmid to produce targeting construct pGA402. Nucleotides 279-3311 of SEQ ID NO:12 was designated SEQ ID NO:14. The fragment was inserted upstream of a CMV promoter and a neomycin

resistance gene and is schematically represented in Fig. 5. For the second targeting sequence of Fig. 5, a DNA fragment containing nucleotides -68 to 69 of the IFNA2 gene sequence shown in Fig. 1 was cloned downstream of the CMV promoter and neomycin resistance gene. Nucleotides -68 to 69 of the IFNA2 gene was designated SEQ ID NO:15. The pGA402 plasmid was introduced into human fibroblast cells exhibiting little or no INFA2 gene expression, to allow homologous recombination with the endogenous INFA2 gene. Cells resistant to G418 after plasmid introduction were screened to identify cells with increased INFA2 gene expression, as would be expected if a homologous recombination event between pGA402 and the genomic DNA took place in the vicinity of the endogenous INFA2 gene.

General Methodologies

Alteration of Endogenous IFNA2 Expression

Using the above-described IFNA2 upstream sequences, one can alter the expression of an endogenous human IFNA2 gene by a method as generally described in U.S. Patent No. 5,641,670. One strategy is shown in Fig. 5. In this strategy, a targeting construct is designed to include a first targeting sequence homologous to a first target site upstream of the gene, an amplifiable marker gene, a selectable marker gene, a regulatory region, a CAP site, an exon, a splice-donor site, an intron, a splice-acceptor site, and a second targeting sequence homologous to a second target site downstream of the first target site and terminating either within or upstream of the IFNA2-coding sequence. According to this strategy, the 5' end of the second target site is preferably less than 107 bp upstream of the normal IFNA2 translational initiation site, in order to avoid undesired ATG start

codons within the transcribed sequence. A transcript produced from the homologously recombined locus will include the construct-derived exon, the construct-derived splice-donor site, the construct-derived intron, the construct-derived splice-acceptor site, any sequence between any of those elements, and the sequence from the construct derived splice acceptor site through the entire endogenous coding sequence to the transcription termination site of the IFNA2 gene. Splicing of this transcript will generate a mRNA which can be translated to produce a precursor of human IFNA2, having either the normal IFNA2 secretion signal sequence or a genetically engineered secretion signal sequence, depending on the characteristics of the construct-derived exon. The size of the exogenous intron and thus the position of the exogenous regulatory region relative to the coding region of the gene can be varied to optimize the function of the regulatory region.

In any activation strategy, the first and second target sites need not be immediately adjacent or even be near each other. When they are not immediately adjacent to each other, a portion of the IFNA2 gene's normal upstream region and/or a portion of the coding region would be deleted upon homologous recombination.

Mutations that facilitate alteration of endogenous IFNA2 expression may be introduced into the chromosomal DNA via homologous recombination. For instance, it may be desirable to abolish a spurious and undesired ATG initiation codon upstream of the correct ATG initiation codon and between the exogenous regulatory region and the endogenous IFNA2 coding region in the homologously recombined locus. To do so, one can employ a targeting construct having a targeting sequence homologous to a genomic site that spans the undesired ATG initiation codon. This targeting sequence contains nucleotides that

correspond to the desired mutation, e.g., contains ATT instead of ATG. The targeting construct optionally includes one or more selectable markers to facilitate selection of homologously recombined cells. An exogenous regulatory region can then be introduced to the homologously recombined cells upstream of the altered sites, using the expression alteration method of the invention.

Alternatively, the exogenous regulatory region and the desired sequence mutation(s) may be introduced into the genomic DNA in a single step. The DNA construct used in this embodiment may contain both the exogenous regulatory region and a targeting sequence that contains nucleotides corresponding to the desired mutation(s). One may also co-transfect or co-infect two separate constructs into target cells, with one construct containing the regulatory region and the other containing nucleotides corresponding to the desired mutation.

If desired, a mammalian splice-acceptor site may be introduced into the genomic DNA, e.g., at a site between an undesired ATG initiation codon and the correct ATG initiation codon, in a similar manner. The DNA construct used for this purpose contains a targeting sequence homologous to a genomic site upstream of the correct INFA2 initiation codon, and adjacent to or embedded within the homologous sequence, a sequence corresponding to the desired splice-acceptor site. Cells containing the correctly recombined IFNA2 locus are then transfected or infected with a second construct containing an exogenous regulatory region and an exon with an unpaired splice-donor site at its 3′ end, together with targeting sequence(s) which target the second construct to a genomic region upstream of the inserted splice-acceptor site. A primary transcript produced under the control of the exogenous regulatory

region will include the exogenous exon, the exogenous splice-donor site, the exogenous splice-acceptor site, any sequences between those elements, and the sequence between the exogenous splice-acceptor site and the transcriptional termination site of the endogenous IFNA2 gene. Upon splicing, the splice-donor site of the transcript will be spliced to the splice-acceptor site, and the intervening intronic RNA, which may contain undesirable AUG initiation codons, will be removed. Any problems associated with having a transcript with undesired AUG translation initiation codons between the transcription start site and the IFNA2-coding sequence are thereby avoided. Of course, the regulatory region, exon, splice donor site, and splice-acceptor site can instead be introduced in a single step. The DNA construct used in this embodiment contains a regulatory region, an exon, a splice-donor site, an intron, a splice-acceptor site, a targeting sequence homologous to a genomic site between the correct INFA2 initiation codon and the undesired ATG codon, and optionally, one or more selectable markers. Alternatively, two separate targeting constructs may be useful, with one containing the regulatory region, the exon, and the splice-donor site, and the other containing the splice-acceptor site. The two constructs can be introduced into target cells in a single step.

The DNA Construct

The DNA construct of the invention includes at least a targeting sequence and a regulatory sequence. It can additionally include an exon; or an exon and splice donor site; or an exon, a splice-donor site, an intron, and a splice-acceptor site. In the construct, the exon, if present, is 3' of the regulatory sequence, and the splice-donor site, if present, is at the 3' end of the exon. The intron and splice acceptor site, if present,

are 3' of the splice donor site. In addition, there can be multiple exons and introns (with appropriate splice donor and acceptor sites) in the construct. The DNA in the construct is referred to as exogenous, since the DNA is not an original part of the genome of a host cell. Exogenous DNA may possess sequences identical to or different from portions of the endogenous genomic DNA present in the cell prior to transfection or infection by viral vector. As used herein, "transfection" means introduction of a plasmid into a cell by nonviral (e.g., chemical or physical) means, such as calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, electroporation, microinjection, microprojectiles, or biolistic-mediated uptake. "Infection" means introduction of a viral vector into a cell by viral infection. Various elements included in the DNA construct of the invention are described in detail below.

The DNA construct can also include *cis*-acting or *trans*-acting viral sequences (e.g., packaging signals), thereby enabling delivery of the construct into the nucleus of a cell via infection by a viral vector. Where necessary, the DNA construct can be disengaged from various steps of a virus life cycle, such as integrase-mediated integration in retroviruses or episome maintenance. Disengagement can be accomplished by appropriate deletions or mutations of viral sequences, such as a deletion of the integrase coding region in a retrovirus vector. Additional details regarding the construction and use of viral vectors are found in Robbins et al., Pharmacol. Ther. 80:35-47, 1998; and Gunzburg et al., Mol. Med. Today 1:410-417, 1995, herein incorporated by reference.

Targeting Sequences

Targeting sequences permit homologous recombination of a desired sequence into a selected site in the host genome. Targeting sequences are homologous to (i.e., able to homologously recombine with) their respective target sites in the host genome.

A circular DNA construct can employ a single targeting sequence, or two or more separate targeting sequences. A linear DNA construct may contain two or more separate targeting sequences. The target site to which a given targeting sequence is homologous can reside within the coding region of the IFNA2 gene, upstream of and immediately adjacent to the coding region, or upstream of and at a distance from the coding region.

The first of the two targeting sequences in the construct (or the entire targeting sequence, if there is only one targeting sequence in the construct) is derived from the newly disclosed genomic regions upstream of the IFNA2-coding sequence. This targeting sequence contains a portion (e.g., 20 or more contiguous nucleotides) of SEQ ID NO:12, e.g., a portion of SEQ ID NO:7, 8, or 13.

The second of the two targeting sequences in the construct may target a genomic region upstream of the coding sequence or target part or all of the coding sequence itself. By way of example, the second targeting sequence may contain, at its 3' end, an "exogenous" coding region identical to the first few codons of the IFNA2 coding sequences. Upon homologous recombination, the exogenous coding region recombines with the targeted part of the endogenous IFNA2-coding sequence. If desired, the exogenous coding region may encode a heterologous amino acid sequence, so long as the exogenous coding region remains sufficiently homologous to the endogenous coding region it replaces to permit homologous recombination.

The targeting sequence may additionally include sequence derived from a previously disclosed region of the IFNA2 gene, including those described herein, as well as a region further upstream which is structurally uncharacterized but can be mapped by one skilled in the art.

Genomic fragments useful as targeting sequences can be identified by their ability to hybridize to a probe containing all or a portion of SEQ ID NO:12. Such a probe can be generated by PCR using primers derived from SEQ ID NO:12.

The Regulatory Sequence

The regulatory sequence of the DNA construct can contain one or more promoters (e.g., a constitutive, tissue-specific, or inducible promoter), enhancers, scaffold-attachment regions or matrix attachment sites, negative regulatory elements, transcription factor binding sites, or combinations of these elements.

The regulatory sequence can be derived from a eukaryotic (e.g., mammalian) or viral genome. Useful regulatory sequences include, but are not limited to, those that regulate the expression of SV40 early or late genes, cytomegalovirus genes, and adenovirus major late genes. They also include regulatory regions derived from genes encoding mouse metallothionein-I, elongation factor-1α, collagen (e.g., collagen Iα1, collagen Iα2, and collagen IV), actin (e.g., γ-actin), immunoglobulin, HMG-CoA reductase, glyceraldehyde phosphate dehydrogenase, 3-phosphoglyceratekinase, collagenase, stromelysin, fibronectin, vimentin, plasminogen activator inhibitor I, thymosin β4, tissue inhibitors of metalloproteinase, ribosomal proteins, major histocompatibility complex molecules, and human leukocyte antigens.

The regulatory sequence preferably contains a transcription factor binding site, such as a TATA Box, CCAAT Box, AP1, Sp1, or a NF-κB binding site.

Marker Genes

If desired, the construct can include a sequence encoding a desired polypeptide, operatively linked to its own promoter. An example of this would be a selectable marker gene, which can be used to facilitate the identification of a targeting event. An amplifiable marker gene can also be included and used to facilitate selection of cells having co-amplified flanking DNA sequences. Cells containing amplified copies of the amplifiable marker gene can be identified by growth in the presence of an agent that selects for the expression of the amplifiable gene. The activated endogenous IFNA2 gene will be amplified in tandem with the amplified selectable marker gene. Cells containing multiple copies of the activated endogenous gene may produce very high levels of IFNA2 and are thus useful for *in vitro* protein production and gene therapy.

The selectable and amplifiable marker genes do not have to lie immediately adjacent to each other. The amplifiable marker gene and selectable marker gene can be the same gene. One or both of the marker genes can be situated in the intron of the DNA construct. Suitable amplifiable marker genes and selectable marker genes are described in U.S. Patent No. 5,641,670.

The Splice-Donor and Splice-Acceptor Sites

The DNA construct may further contain an exon, a splice-donor site at the 3′ end of the exon, an intron, and a splice-acceptor site.

A splice-donor site is a sequence which directs the splicing of one exon of an RNA transcript to the splice-acceptor site of another exon of the transcript,

resulting in removal of the intron between the two sites. Typically, the first exon lies 5′ of the second exon, and the splice-donor site located at the 3′ end of the first exon is paired with a splice-acceptor site flanking the second exon on the 5′ side of the second exon. Splice-donor sites have a characteristic consensus sequence represented as (A/C)AGGURAGU (where R denotes a purine nucleotide), with the GU in the fourth and fifth positions being required (Jackson, Nucleic Acids Research 19: 3715-3798, 1991). The first three bases of the splice-donor consensus site are the last three bases of the exon: i.e., they are not spliced out. Splice-donor sites are functionally defined by their ability to effect the appropriate reaction within the mRNA splicing pathway.

A splice acceptor site in a construct of the invention directs, in conjunction with a splice donor site, the splicing of one exon to another exon. Splice-acceptor sites have a characteristic sequence represented as $(Y)_nNYAG$ (SEQ ID NO:10), where Y denotes any pyrimidine and N denotes any nucleotide (Jackson, Nucleic Acids Research 19:3715-3798, 1991).

The CAP Site

The DNA construct can optionally contain a CAP site. A CAP site is a specific transcription start site which is associated with and utilized by the regulatory region. This CAP site is located at a position relative to the regulatory sequence in the construct such that following homologous recombination, the regulatory sequence directs synthesis of a transcript that begins at the CAP site. Alternatively, no CAP site is included in the construct, and the transcriptional apparatus will locate by default an appropriate site in the targeted gene to be utilized as a CAP site.

Additional DNA elements

The construct may additionally contain sequences which affect the structure or stability of the RNA or protein produced by homologous recombination. Optionally, the DNA construct can include a bacterial origin of replication and bacterial antibiotic resistance markers or other selectable markers, which allow for large-scale plasmid propagation in bacteria or any other suitable cloning/host system.

All of the above-described elements of the DNA construct are operatively linked or functionally placed with respect to each other. That is, upon homologous recombination between the construct and the targeted genomic DNA, the regulatory sequence can direct the production of a primary RNA transcript which initiates at a CAP site (optionally included in the construct) and includes the sequence lying between the CAP site and the endogenous IFNA2 gene's transcription stop site. Depending on the location of the CAP site, a portion of this sequence may include the IFNA2 gene's endogenous regulatory region as well as sequences neighboring that region that are normally not transcribed. If an exon, a splice-donor site and a splice-acceptor site are present in the construct, the primary transcript will also include the exon, the two splice sites, and the intron between the two sites.

The order of elements in the DNA construct can vary. Where the construct is a circular plasmid or viral vector, the relative order of elements in the resulting structure can be, for example: a targeting sequence, plasmid DNA (comprised of sequences used for the selection and/or replication of the targeting plasmid in a microbial or other suitable host), selectable marker(s), a regulatory sequence, an exon, a splice-donor site, an intron, and a splice-acceptor site.

Where the construct is linear, the order can be, for example: a first targeting sequence, a selectable marker gene, a regulatory sequence, an exon, a splice-donor site, an intron, a splice-acceptor site, and a second targeting sequence; or, in the alternative, a first targeting sequence, a regulatory sequence, an exon, a splice-donor site, an intron, a splice-acceptor site, a selectable marker gene, optionally an internal ribosomal entry site, and a second targeting sequence.

Alternatively, the order can be: a first targeting sequence, a first selectable marker gene, a regulatory sequence, an exon, a splice-donor site, an intron, a splice-acceptor site, a second targeting sequence, and a second selectable marker gene; or, a first targeting sequence, a regulatory sequence, an exon, a splice-donor site, an intron, a splice-acceptor site, a first selectable marker gene, a second targeting sequence, and a second selectable marker gene. Recombination between the targeting sequences flanking the first selectable marker with homologous sequences in the host genome results in the targeted integration of the first selectable marker, while the second selectable marker is not integrated. Desired transfected or infected cells are those that are stably transfected or infected with the first, but not second, selectable marker. Such cells can be selected for by growth in a medium containing an agent which selects for expression of the first marker and another agent which selects against the second marker. Transfected or infected cells that have improperly integrated the targeting construct by a mechanism other than homologous recombination would be expected to express the second marker gene and will thereby be killed in the selection medium.

A positively selectable marker is sometimes included in the construct to allow for the selection of

cells containing amplified copies of that marker. In this embodiment, the order of construct components can be, for example: a first targeting sequence, an amplifiable positively selectable marker, a second selectable marker (optional), a regulatory sequence, an exon, a splice-donor site, an intron, a splice-acceptor site, and a second targeting DNA sequence.

The various elements of the construct can be obtained from natural sources (e.g., genomic DNA), or can be produced using genetic engineering techniques or synthetic processes. The regulatory region, CAP site, splice-donor site, intron, and splice acceptor site of the construct can be isolated as a complete unit from, e.g., the human elongation factor-1α (Genbank sequence HUMEF1A) gene or the cytomegalovirus (Genbank sequence HEHCMVP1) immediate early region. These components can also be isolated from separate genes.

Transfection or Infection and Homologous Recombination

The DNA construct of the invention can be introduced into the cell, such as a primary, secondary, or immortalized cell, as a single DNA construct, or as separate DNA sequences which become incorporated into the chromosomal or nuclear DNA of a transfected or infected cell. By "transfected cell" is meant a cell into which (or into an ancestor of which) a DNA or RNA molecule has been introduced by a means other than using a viral vector. By "infected cell" is meant a cell into which (or into an ancestor of which) a DNA or RNA molecule has been introduced using a viral vector. Viruses known to be useful as vectors include adenovirus, adeno-associated virus, Herpes virus, mumps virus, poliovirus, lentivirus, retroviruses, Sindbis virus, and vaccinia viruses such as canary pox virus. The DNA can be introduced as a linear, double-stranded (with or without single-stranded regions at one or both ends), single-stranded, or circular

molecule. When the construct is introduced into host cells in two separate DNA fragments, the two fragments share DNA sequence homology (overlap) at the 3' end of one fragment and the 5' end of the other, while one carries a first targeting sequence and the other carries a second targeting sequence. Upon introduction into a cell, the two fragments can undergo homologous recombination to form a single molecule with the first and second targeting sequences flanking the region of overlap between the two original fragments. The product molecule is then in a form suitable for homologous recombination with the cellular target sites. More than two fragments can be used, with each of them designed such that they will undergo homologous recombination with each other to ultimately form a product suitable for homologous recombination with the cellular target sites as described above.

The DNA construct of the invention, if not containing a selectable marker itself, can be co-transfected or co-infected with another construct that contains such a marker. A targeting plasmid may be cleaved with a restriction enzyme at one or more sites to create a linear or gapped molecule prior to transfection or infection. The resulting free DNA ends increase the frequency of the desired homologous recombination event. In addition, the free DNA ends may be treated with an exonuclease to create overhanging 5' or 3' single-stranded DNA ends (e.g., at least 30 nucleotides in length, and preferably 100-1000 nucleotides in length) to increase the frequency of the desired homologous recombination event. In this embodiment, homologous recombination between the targeting sequence and the genomic target will result in two copies of the targeting sequences, flanking the elements contained within the introduced plasmid.

The DNA constructs may be transfected into cells (preferably *in vitro*) by a variety of physical or chemical methods, including electroporation, microinjection, microprojectile bombardment, calcium phosphate precipitation, liposome delivery, or polybrene- or DEAE dextran-mediated transfection.

The transfected or infected cell is maintained under conditions which permit homologous recombination, as described in the art (see, e.g., Capecchi, Science 24:1288-1292, 1989). When the homologously recombinant cell is maintained under conditions sufficient to permit transcription of the DNA, the regulatory region introduced by the DNA construct will alter transcription of the IFNA2 gene.

Homologously recombinant cells (i.e., cells that have undergone the desired homologous recombination) can be identified by phenotypic screening or by analyzing the culture supernatant in enzyme-linked immunosorbent assays (ELISA) for IFNA2. Commercial ELISA kits for detecting IFNA2 are available from Biosource International (Camarillo, CA). Homologously recombinant cells can also be identified by Southern and Northern analyses or by polymerase chain reaction (PCR) screening.

As used herein, the term "primary cells" includes (i) cells present in a suspension of cells isolated from a vertebrate tissue source (prior to their being plated, i.e., attached to a tissue culture substrate such as a dish or flask), (ii) cells present in an explant derived from tissue, (iii) cells plated for the first time, and (iv) cell suspensions derived from these plated cells. Primary cells can also be cells as they naturally occur within a human or an animal.

Secondary cells are cells at all subsequent steps in culturing. That is, the first time that plated primary cells are removed from the culture substrate and

replated (passaged), they are referred to herein as secondary cells, as are all cells in subsequent passages. Secondary cell strains consist of secondary cells which have been passaged one or more times. Secondary cells typically exhibit a finite number of mean population doublings in culture and the property of contact-inhibited, anchorage-dependent growth (anchorage-dependence does not apply to cells that are propagated in suspension culture). Primary and secondary cells are not immortalized

Immortalized cells are cell lines (as opposed to cell strains, with the designation "strain" reserved for primary and secondary cells) that exhibit an apparently unlimited lifespan in culture.

Cells selected for transfection or infection can fall into four types or categories: (i) cells which do not, as obtained, make or contain more than trace amounts of the IFNA2 protein, (ii) cells which make or contain the protein but in quantities other than those desired (such as, in quantities less than the level which is physiologically normal for the type of cells as obtained), (iii) cells which make the protein at a level which is physiologically normal for the type of cells as obtained, but are to be augmented or enhanced in their content or production, and (iv) cells in which it is desirable to change the pattern of regulation or induction of a gene encoding the protein.

Primary, secondary and immortalized cells to be transfected or infected by the present method can be obtained from a variety of tissues and include all appropriate cell types which can be maintained in culture. For example, suitable primary and secondary cells include fibroblasts, keratinocytes, epithelial cells (e.g., mammary epithelial cells, intestinal epithelial cells), endothelial cells, glial cells, neural

cells, formed elements of the blood (e.g., lymphocytes, bone marrow cells), muscle cells, and precursors of these somatic cell types. Where the homologously recombinant cells are to be used in gene therapy, primary cells are preferably obtained from the individual to whom the transfected or infected primary or secondary cells are to be administered. However, primary cells can be obtained from a donor (i.e., an individual other than the recipient) of the same species.

Examples of immortalized human cell lines useful for protein production or gene therapy include, but are not limited to, 2780AD ovarian carcinoma cells (Van der Blick et al., Cancer Res., 48:5927-5932, 1988), A549 (American Type Culture Collection ("ATCC") CCL 185), BeWo (ATCC CCL 98), Bowes Melanoma cells (ATCC CRL 9607), CCRF-CEM (ATCC CCL 119), CCRF-HSB-2 (ATCC CCL 120.1), COLO201 (ATCC CCL 224), COLO205 (ATCC CCL 222), COLO 320DM (ATCC CCL 220), COLO 320HSR (ATCC CCL 220.1), Daudi cells (ATCC CCL 213), Detroit 562 (ATCC CCL 138), HeLa cells and derivatives of HeLa cells (ATCC CCL 2, 2.1 and 2.2), HCT116 (ATCC CCL 247), HL-60 cells (ATCC CCL 240), HT1080 cells (ATCC CCL 121), IMR-32 (ATCC CCL 127), Jurkat cells (ATCC TIB 152), K-562 leukemia cells (ATCC CCL 243), KB carcinoma cells (ATCC CCL 17), KG-1 (ATCC CCL 246), KG-1a (ATCC CCL 246.1), LS123 (ATCC CCL 255), LS174T (ATCC CCL CL-188), LS180 (ATCC CCL CL-187), MCF-7 breast cancer cells (ATCC BTH 22), MOLT-4 cells (ATCC CRL 1582), Namalwa cells (ATCC CRL 1432), NCI-H498 (ATCC CCL 254), NCI-H508 (ATCC CCL 253), NCI-H548 (ATCC CCL 249), NCI-H716 (ATCC CCL 251), NCI-H747 (ATCC CCL 252), NCI-H1688 (ATCC CCL 257), NCI-H2126 (ATCC CCL 256), Raji cells (ATCC CCL 86), RD (ATCC CCL 136), RPMI 2650 (ATCC CCL 30), RPMI 8226 cells (ATCC CCL 155), SNU-C2A (ATCC CCL 250.1), SNU-C2B (ATCC CCL 250), SW-13 (ATCC CCL 105), SW48 (ATCC CCL 231), SW403 (ATCC CCL 230), SW480 (ATCC

CCL 227), SW620 (ATCC CCL 227), SW837 (ATCC CCL 235), SW948 (ATCC CCL 237), SW1116 (ATCC CCL 233), SW1417 (ATCC CCL 238), SW1463 (ATCC CCL 234), T84 (ATCC CCL 248), U-937 cells (ATCC CRL 1593), WiDr (ATCC CCL 218), and WI-38VA13 subline 2R4 cells (ATCC CLL 75.1), as well as heterohybridoma cells produced by fusion of human cells and cells of another species. Secondary human fibroblast strains, such as WI-38 (ATCC CCL 75) and MRC-5 (ATCC CCL 171), may be used. In addition, primary, secondary, or immortalized human cells, as well as primary, secondary, or immortalized cells from other species, can be used for *in vitro* protein production or gene therapy.

IFNA2-Expressing Cells

Homologously recombinant cells of the invention express IFNA2 at desired levels and are useful for both *in vitro* production of IFNA2 and gene therapy.

Protein Production

Homologously recombinant cells according to this invention can be used for *in vitro* production of IFNA2. The cells are maintained under conditions, as described in the art, which result in expression of proteins. The IFNA2 protein may be purified from cell lysates or cell supernatants. A pharmaceutical composition containing the IFNA2 protein can be delivered to a human or an animal by conventional pharmaceutical routes known in the art (e.g., oral, intravenous, intramuscular, intranasal, pulmonary, transmucosal, intradermal, rectal, intrathecal, transdermal, subcutaneous, intraperitoneal, or intralesional). Oral administration may require use of a strategy for protecting the protein from degradation in the gastrointestinal tract: e.g., by encapsulation in polymeric microcapsules.

Gene Therapy

Homologously recombinant cells of the present invention are useful as populations of homologously

recombinant cell lines, as populations of homologously recombinant primary or secondary cells, as homologously recombinant clonal cell strains or lines, as homologously recombinant heterogenous cell strains or lines, and as cell mixtures in which at least one representative cell of one of the four preceding categories of homologously recombinant cells is present. Such cells may be used in a delivery system for treating (i) infections caused by such viruses as papilloma virus, hepatitis B and C viruses, vaccinia, herpes simplex virus, herpes zoster varicellosus virus, and rhinovirus, and (ii) any other conditions treatable with IFNA2.

Homologously recombinant primary cells, clonal cell strains or heterogenous cell strains are administered to an individual in whom the abnormal or undesirable condition is to be treated or prevented, in sufficient quantity and by an appropriate route, to express or make available the protein or exogenous DNA at physiologically relevant levels. A physiologically relevant level is one which either approximates the level at which the product is normally produced in the body or results in improvement of the abnormal or undesirable condition. If the cells are syngeneic with respect to a immunocompetent recipient, the cells can be administered or implanted intravenously, intraarterially, subcutaneously, intraperitoneally, intraomentally, subrenal capsularly, intrathecally, intracranially, or intramuscularly.

If the cells are not syngeneic and the recipient is immunocompetent, the homologously recombinant cells to be administered can be enclosed in one or more semipermeable barrier devices. The permeability properties of the device are such that the cells are prevented from leaving the device upon implantation into a subject, but the therapeutic protein is freely

permeable and can leave the barrier device and enter the local space surrounding the implant or enter the systemic circulation. See, e.g., U.S. Patent Nos. 5,641,670, 5,470,731, 5,620,883, 5,487,737, and co-owned U.S. Patent Application entitled "Delivery of Therapeutic Proteins" (inventors: Justin C. Lamsa and Douglas A. Treco), filed April 16, 1999, all herein incorporated by reference. The barrier device can be implanted at any appropriate site: e.g., intraperitoneally, intrathecally, subcutaneously, intramuscularly, within the kidney capsule, or within the omentum.

Barrier devices are particularly useful and allow homologously recombinant immortalized cells, homologously recombinant cells from another species (homologously recombinant xenogeneic cells), or cells from a nonhistocompatibility-matched donor (homologously recombinant allogeneic cells) to be implanted for treatment of a subject. The devices retain cells in a fixed position *in vivo*, while protecting the cells from the host's immune system. Barrier devices also allow convenient short-term (i.e., transient) therapy by allowing ready removal of the cells when the treatment regimen is to be halted for any reason. Transfected or infected xenogeneic and allogeneic cells may also be used in the absence of barrier devices for short-term gene therapy. In that case, the IFNA2 produced by the cells will be delivered *in vivo* until the cells are rejected by the host's immune system.

A number of synthetic, semisynthetic, or natural filtration membranes can be used for this purpose, including, but not limited to, cellulose, cellulose acetate, nitrocellulose, polysulfone, polyvinylidene difluoride, polyvinyl chloride polymers and polymers of polyvinyl chloride derivatives. Barrier devices can be utilized to allow primary, secondary, or immortalized

cells from another species to be used for gene therapy in humans.

Another type of device useful in the gene therapy of the invention is an implantable collagen matrix in which the cells are embedded. Such a device, which can contain beads to which the cells attach, is described in WO 97/15195, herein incorporated by reference. It can be implanted as described above.

The number of cells needed for a given dose or implantation depends on several factors, including the expression level of the protein, the size and condition of the host animal, and the limitations associated with the implantation procedure. Usually the number of cells implanted in an adult human or other similarly-sized animal is in the range of 1×10^4 to 5×10^{10}, and preferably 1×10^8 to 1×10^9. If desired, they may be implanted at multiple sites in the patient, either at one time or over a period of months or years. The dosage may be repeated as needed.

Deposit

Under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure, the deposit of plasmid pA2HB was made with the American Type Culture Collection (ATCC) of Rockville, MD, USA on May 12, 1998. The deposit was given Accession Number 209872.

Applicants' assignee, Transkaryotic Therapies, Inc., represents that the ATCC is a depository affording permanence of the deposit and ready accessibility thereto by the public if a patent is granted. All restrictions on the availability to the public of the material so deposited will be irrevocably removed upon the granting of the patent. The material will be available during the pendency of the patent application to one determined by the Commissioner to be entitled thereto under 37 CFR 1.14

and 35 U.S.C. §122. The deposited material will be maintained with all the care necessary to keep it viable and uncontaminated for a period of at least five years after the most recent request for the furnishing of a sample of the deposited material, and in any case, for a period of at least thirty (30) years after the date of deposit or for the enforceable life of the patent, whichever period is longer. Applicants' assignee acknowledges its duty to replace the deposit should the depository be unable to furnish a sample when requested due to the condition of the deposit.

Other Embodiments

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not to limit the scope of the invention, which is defined by the scope of the appended claims.

Other aspects, advantages, and modifications are within the scope of the following claims.

What is claimed is:

1. A DNA construct that alters expression of an endogenous IFNA2 gene in a mammalian cell upon integration into the genome of the cell via homologous recombination, the construct comprising (i) a targeting sequence containing at least 20 contiguous nucleotides of SEQ ID NO:12, and (ii) a transcriptional regulatory sequence.

2. The DNA construct of claim 1, wherein the construct further comprises an exon, a splice-donor site, an intron and a splice-acceptor site.

3. The DNA construct of claim 1, wherein the construct further comprises a selectable marker gene.

4. The DNA construct of claim 1, wherein the targeting sequence contains at least 50 contiguous nucleotides of SEQ ID NO:12.

5. A DNA construct that alters expression of an endogenous IFNA2 gene in a mammalian cell upon integration into the genome of the cell via homologous recombination, the construct comprising (i) a targeting sequence containing at least 20 contiguous nucleotides of SEQ ID NO:7, and (ii) a transcriptional regulatory sequence.

6. The DNA construct of claim 5, wherein the construct further comprises an exon, a splice-donor site, an intron and a splice-acceptor site.

7. A DNA construct that alters expression of an endogenous IFNA2 gene in a mammalian cell upon integration into the genome of the cell via homologous recombination, the construct comprising (i) a targeting sequence containing at least 20 contiguous nucleotides of SEQ ID NO:8, and (ii) a transcriptional regulatory sequence.

8. The DNA construct of claim 7, wherein the construct further comprises an exon, a splice-donor site, an intron and a splice-acceptor site.

9. An isolated nucleic acid comprising at least 20 contiguous nucleotides of SEQ ID NO:12 or its complement, wherein the isolated nucleic acid does not encode full-length interferon-α 2.

10. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises at least 50 contiguous nucleotides of SEQ ID NO:12 or its complement.

11. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises at least 100 contiguous nucleotides of SEQ ID NO:12 or its complement.

12. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises at least 200 contiguous nucleotides of SEQ ID NO:12 or its complement.

13. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises SEQ ID NO:7 or its complement.

14. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises SEQ ID NO:8 or its complement.

15. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises SEQ ID NO:12 or its complement.

16. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises at least 20 contiguous nucleotides of SEQ ID NO:7 or its complement.

17. The isolated nucleic acid of claim 9, wherein the isolated nucleic acid comprises at least 20 contiguous nucleotides of SEQ ID NO:8 or its complement.

18. An isolated nucleic acid comprising a strand that comprises a nucleotide sequence that (i) is at least 100 nucleotides in length and (ii) hybridizes under highly stringent conditions with SEQ ID NO:12, or the complement of SEQ ID NO:12.

19. The isolated nucleic acid of claim 18, wherein the nucleotide sequence is at least 200 nucleotides in length.

20. The isolated nucleic acid of claim 18, wherein the nucleotide sequence is at least 400 nucleotides in length.

21. The isolated nucleic acid of claim 18, wherein the nucleotide sequence is at least 1,000 nucleotides in length.

22. An isolated nucleic acid comprising a strand that comprises a nucleotide sequence that (i) is at least 100 nucleotides in length and (ii) hybridizes under highly stringent conditions with SEQ ID NO:7, or the complement of SEQ ID NO:7.

23. An isolated nucleic acid comprising a strand that comprises a nucleotide sequence that (i) is at least 50 nucleotides in length and (ii) hybridizes under highly stringent conditions with SEQ ID NO:8, or the complement of SEQ ID NO:8.

24. An isolated nucleic acid comprising a strand that comprises a nucleotide sequence that (i) is at least 50 nucleotides in length and (ii) shares at least 80% sequence identity with a fragment of SEQ ID NO:12 having the same length as the nucleotide sequence.

25. The isolated nucleic acid of claim 24, wherein the nucleotide sequence is at least 100 nucleotides in length.

26. The isolated nucleic acid of claim 24, wherein the fragment is a part or all of SEQ ID NO:7.

27. The isolated nucleic acid of claim 24, wherein the fragment is a part or all of SEQ ID NO:8.

28. A homologously recombinant mammalian cell stably transfected with the DNA construct of claim 1, the DNA construct having undergone homologous recombination with genomic DNA upstream of the ATG initiation codon of an endogenous IFNA2 coding sequence.

29. A homologously recombinant mammalian cell stably transfected with the DNA construct of claim 2, the DNA construct having undergone homologous recombination with genomic DNA upstream of the ATG initiation codon of an endogenous IFNA2 coding sequence.

30. A homologously recombinant cell stably transfected with the DNA construct of claim 3, the DNA construct having undergone homologous recombination with genomic DNA upstream of the ATG initiation codon of an endogenous IFNA2 coding sequence.

31. A homologously recombinant cell stably transfected with the DNA construct of claim 4, the DNA construct having undergone homologous recombination with genomic DNA upstream of the ATG initiation codon of an endogenous IFNA2 coding sequence.

32. A method of altering expression of an endogenous IFNA2 gene in a mammalian cell, the method comprising introducing the DNA construct of claim 1 into the cell and maintaining the cell under conditions which permit homologous recombination to occur between the construct and a target site 5' to the coding sequence of the endogenous IFNA2 gene.

33. A method of delivering IFNA2 to an animal, comprising

providing the cell of claim 28; and

implanting the cell in the animal, wherein the cell secretes IFNA2.

34. A method of delivering IFNA2 to an animal, comprising

providing the cell of claim 29; and

implanting the cell in the animal, wherein the cell secretes IFNA2.

35. A method of delivering IFNA2 to an animal, comprising

providing the cell of claim 30; and

implanting the cell in the animal, wherein the cell secretes IFNA2.

36. A method of delivering IFNA2 to an animal, comprising

providing the cell of claim 31; and

implanting the cell in the animal, wherein the cell secretes IFNA2.

37. A method of producing IFNA2, comprising

providing the cell of claim 28, and

culturing the cell *in vitro* under conditions which permit the cell to express and secrete IFNA2.

38. A method of producing IFNA2, comprising

providing the cell of claim 29, and

culturing the cell *in vitro* under conditions which permit the cell to express and secrete IFNA2.

39. A method of producing IFNA2, comprising

providing the cell of claim 30, and

culturing the cell *in vitro* under conditions which permit the cell to express and secrete IFNA2.

40. A method of producing IFNA2, comprising providing the cell of claim 31, and culturing the cell *in vitro* under conditions which permit the cell to express and secrete IFNA2.

41. A DNA construct that alters expression of an endogenous IFNA2 gene in a mammalian cell upon integration into the genome of the cell via homologous recombination, the construct comprising (i) a targeting sequence containing at least 20 contiguous nucleotides of one or more of SEQ ID NOs:16, 17, 18, and 19, and (ii) a transcriptional regulatory sequence.

42. An isolated nucleic acid comprising at least 20 contiguous nucleotides of one or more of SEQ ID NOs:16, 17, 18, and 19, or the complement of one or more of SEQ ID NOs: 16, 17, 18, and 19, wherein the isolated nucleic acid does not encode full-length interferon-α 2.

43. A homologously recombinant mammalian cell, stably transfected with the DNA construct of claim 39, the DNA construct having undergone homologous recombination with genomic DNA upstream of the ATG initiation codon of an endogenous IFNA2 coding sequence.

44. A method of altering expression of an endogenous IFNA2 gene in a mammalian cell, the method comprising introducing the DNA construct of claim 39 into the cell and maintaining the cell under conditions which permit homologous recombination to occur between the construct and a target site 5′ to the coding sequence of the endogenous IFNA2 gene.

45. A method of delivering IFNA2 to an animal, comprising

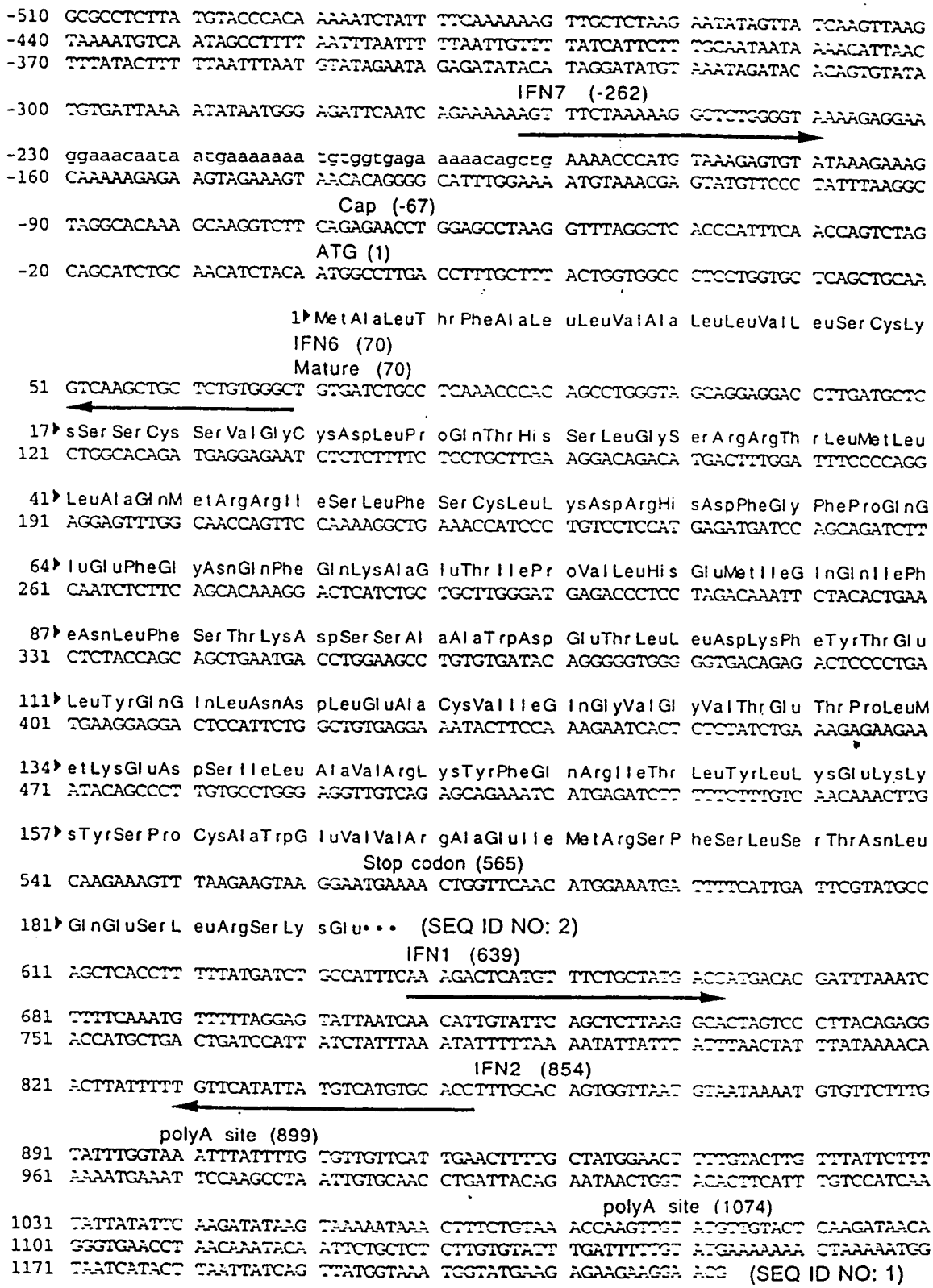
providing the cell of claim 41; and

implanting the cell in the animal, wherein the cell secretes IFNA2.

46. A method of producing IFNA2, comprising

providing the cell of claim 41, and

culturing the cell *in vitro* under conditions which permit the cell to express and secrete IFNA2.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Cap (-67)
ATG (1)
IFN6 (70)
Mature (70)
Stop codon (565)
(SEQ ID NO: 2)
IFN1 (639)
IFN2 (854)
polyA site (899)
polyA site (1074)
(SEQ ID NO: 1)

FIG. 1

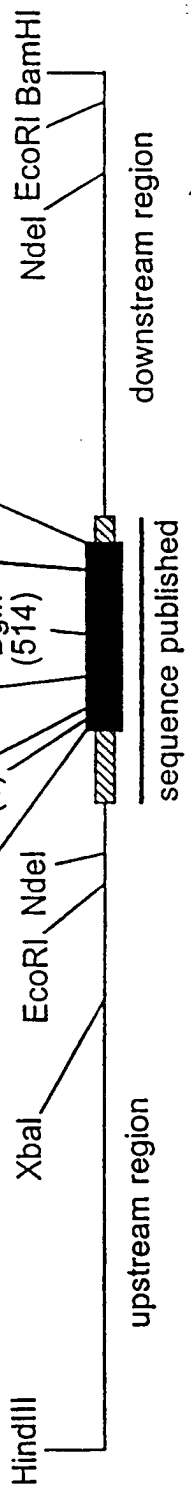
HindIII
upstream region
XbaI
EcoRI
NdeI
Cap (-67)
ATG (1)
Mature (70)
BglII (254)
polyA site (899)
BglII (514)
polyA site (1074)
sequence published
downstream region
NdeI
EcoRI
BamHI

FIG. 2

HindIII

1 AAGCTTTTAT AGGTGTAAAT TTTCCACTTA GTACTGCTTT TGTAATGTTG TCTTTTTATT TTCATTTATC

1 TCAAGATGTT TTCTAATTTC TCTTGACTTC CTTCTTAAAT TCTTACCTCA TGTAGACATA CATTTTTGGC

1 CCTATGCATT GGGATGCAAA ACCAGACTAA TTTACTTTGT ACAAAAAGAA AAATGAGAAA GAAATATATT

1 TGGTCTTGTG AGCACTATAT GGAAATACTT TATATTCCAT TTGTTTCATC ATATTCATAT ATCCCTTT

(SEQ ID NO: 7)

FIG. 3

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-583 CATTGGATAC TCCATCACCT GCTGTGATAT TATGAATGTC TGCCTATATA AATATTCACT ATTCCATAAC

-513 ACAGCGCCTC TTATGTACCC ACAAAAATCT ATTTTCAAAA AAGTTGCTCT AAGAATATAG TTATCAAGTT

-443 AAGTAAAATG TCAATAGCCT TTTAATTTAA TTTTTAATTG TTTTATCATT CTTTGCAATA ATAAAACATT
-373 AACTTTATAC TTTTTAATTT AATGTATAGA ATAGAGATAT ACATAGGATA TGTAAATAGA TACACAGTGT
-303 ATATGTGATT AAAATATAAT GGGAGATTCA ATCAGAAAAA AGTTTCTAAA AAGGCTCTGG GGTAAAAGAG
-233 GAAggaaaca ataatgaaaa aaatgtggtg agaaaaacag ctgAAAACCC ATGTAAAGAG TGTATAAAGA
-163 AAGCAAAAAG AGAAGTAGAA AGTAACACAG GGGCATTTGG AAAATGTAAA CGAGTATGTT CCCTATTTAA

                                Cap (-67)
 -93 GGCTAGGCAC AAAGCAAGGT CTTCAGAGAA CCTGGAGCCT AAGGTTTAGG CTCACCCATT TCAACCAGTC

                              ATG (1)
 -23 TAGCAGCATC TGCAACATCT ACAATGGCCT TGACCTTTGC TTTACTGGTG GCCCTCCTGG TGCTCAGCTG
                           1▶MetAlaL euThrPheAl aLeuLeuVal AlaLeuLeuV alLeuSerCy

                            Mature (70)
  48 CAAGTCAAGC TGCTCTGTGG GCTGTGATCT GCCTCAAACC CACAGCCTGG GTAGCAGGAG GACCTTGATG
  16▶sLysSerSer CysSerValG ly
                           1▶CysAspLe uProGlnThr HisSerLeuG lySerArgAr gThrLeuMet
 118 CTCCTGGCAC AGATGAGGAG AATCTCTCTT TTCTCCTGCT TGAAGGACAG ACATGACTTT GGATTTCCCC

  17▶LeuLeuAlaG lnMetArgAr gIleSerLeu PheSerCysL euLysAspAr gHisAspPhe GlyPheProG

                                                                    BglII  (254)
 188 AGGAGGAGTT TGGCAACCAG TTCCAAAAGG CTGAAACCAT CCCTGTCCTC CATGAGATGA TCCAGCAGAT

  40▶lnGluGluPh eGlyAsnGln PheGlnLysA laGluThrIl eProValLeu HisGluMetI leGlnGlnIl
 258 CTTCAATCTC TTCAGCACAA AGGACTCATC TGCTGCTTGG GATGAGACCC TCCTAGACAA ATTCTACACT

  63▶ePheAsnLeu PheSerThrL ysAspSerSe rAlaAlaTrp AspGluThrL euLeuAspLy sPheTyrThr
 328 GAACTCTACC AGCAGCTGAA TGACCTGGAA GCCTGTGTGA TACAGGGGGT GGGGGTGACA GAGACTCCCC

  87▶GluLeuTyrG lnGlnLeuAs nAspLeuGlu AlaCysVall leGlnGlyVa lGlyValThr GluThrProL
 398 TGATGAAGGA GGACTCCATT CTGGCTGTGA GGAAATACTT CCAAAGAATC ACTCTCTATC TGAAAGAGAA

 110▶euMetLysGl uAspSerIle LeuAlaValA rgLysTyrPh eGlnArgIle ThrLeuTyrL euLysGluLy

                                                    BglII  (514)
 468 GAAATACAGC CCTTGTGCCT GGGAGGTTGT CAGAGCAGAA ATCATGAGAT CTTTTTCTTT GTCAACAAAC

 133▶sLysTyrSer ProCysAlaT rpGluValVa lArgAlaGlu IleMetArgS erPheSerLe uSerThrAsn
 538 TTGCAAGAAA GTTTAAGAAG TAAGGAATGA AAACTGGTTC AACATGGAAA TGATTTTCAT TGATTCGTAT

 157▶LeuGlnGluS erLeuArgSe rLysGlu••• (SEQ ID NO: 2)
 608 GCCAGCTCAC CTTTTTATGA TCTGCCATTT CAAAGACTCA TGTTTCTGCT ATGACCATGA CACGATTTAA
 678 ATCTTTTCAA ATGTTTTTAG GAGTATTAAT CAACATTGTA TTCAGCTCTT AAGGCACTAG TCCCTTACAG
 748 AGGACCATGC TGACTGATCC ATTATCTATT TAAATATTTT TAAAATATTA TTTATTTAAC TATTTATAAA
 818 ACAACTTATT TTTGTTCATA TTATGTCATG TGCACCTTTG CACAGTGGTT AATGTAATAA AATGTGTTCT

                polyA site (899)
 888 TTGTATTTGG TAAATTTATT TTGTGTTGTT CATTGAACTT TTGCTATGGA ACTTTTGTAC TTGTTTATTC
 958 TTTAAAATGA AATTCCAAGC CTAATTGTGC AACCTGATTA CAGAATAACT GGTACACTTC ATTTGTCCAT

                                                    polyA site (1074)
1028 CAATATTATA TTCAAGATAT AAGTAAAAAT AAACTTTCTG TAAACCAAGT TGTATGTTGT ACTCAAGATA
1098 ACAGGGTGAA CCTAACAAAT ACAATTCTGC TCTCTTGTGT ATTTGATTTT TGTATGAAAA AAACTAAAAA
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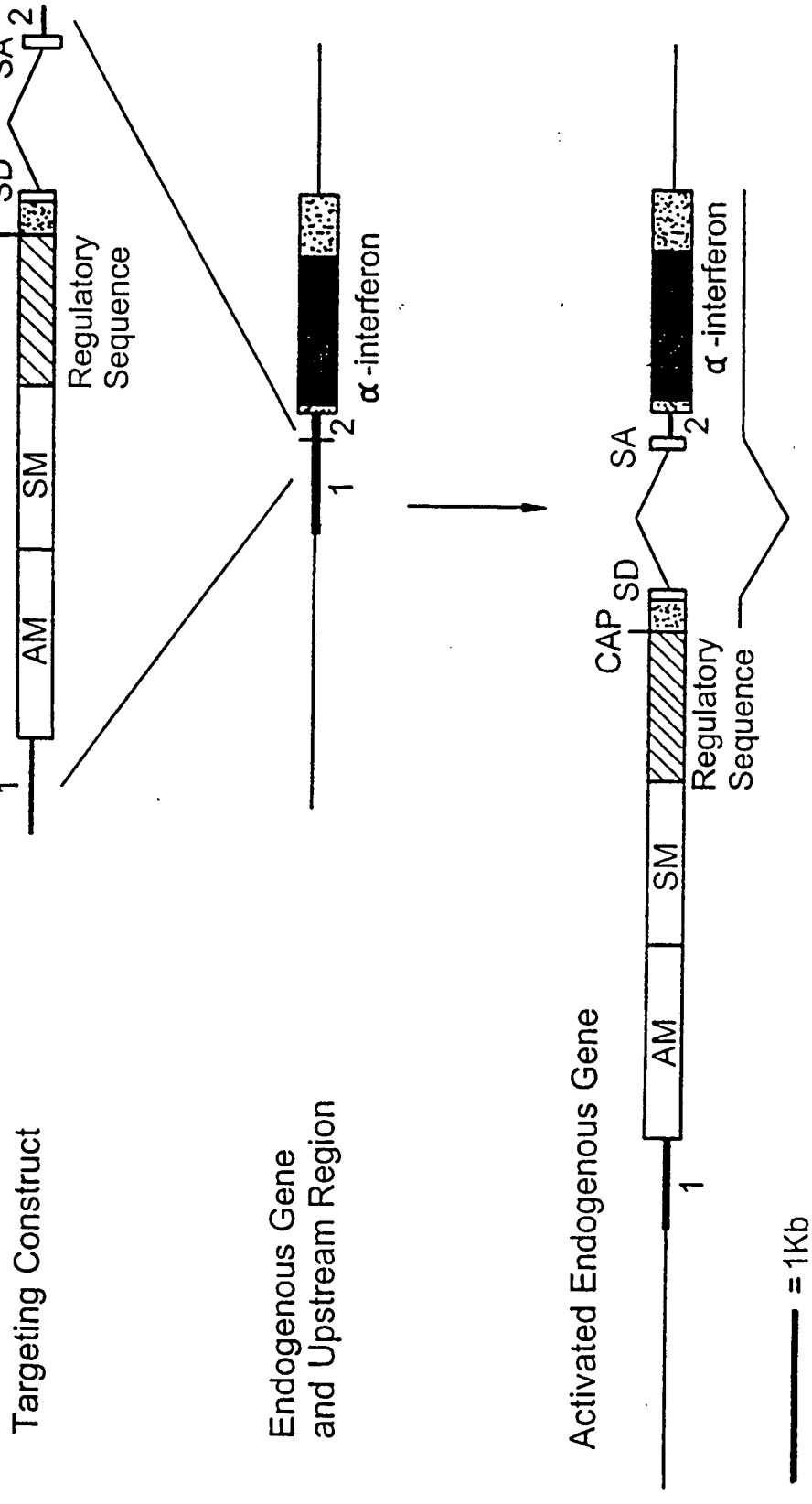
FIG. 4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AM
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FIG. 5

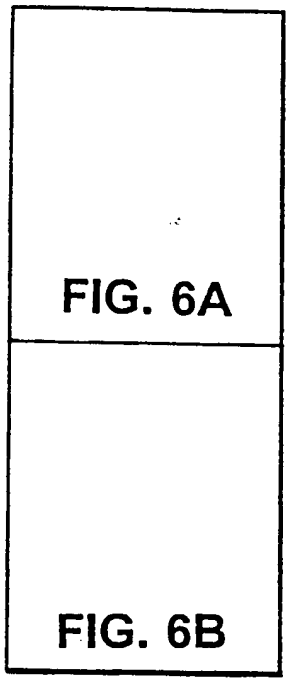

FIG. 6

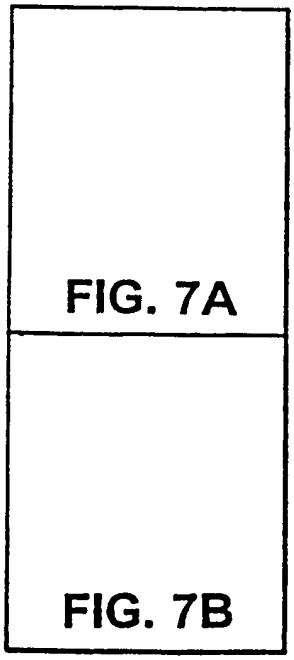

FIG. 7

HindIII (-4073)

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-3954 TGTAGACATA CATTTTTGGC CCTATGCATT GGGATGCAAA ACCAGACTAA TTTACTTTGT
-3894 ACAAAAAGAA AAATGAGAAA GAAATATATT TGGTCTTGTG AGCACTATAT GGAAATACTT
-3834 TATATTCCAT TTGTTTCATC ATATTCATAT ATCCCTTTAC TAACATAAAG CTGAAGGTGA
-3774 ATAAAAAAAT CAGGGTTAGC CAAACAAATT TTCATGGTCA AATACCACAT AAAAAGTAAA
-3714 TATACTTAAG TTCCCAGCAA AATCTGAATT GAACGTAGAC AAAATGCTCA TTTCTCAGTG
-3654 TTTGACAGAC TTAACAGTTT GAGCCAATAA AAATGTACTG ACTAGATAAA CTACTAAAAG
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-3534 TGCCCATTTA AGAACTTTGA GCATTTTAAT TGTTTAATAA TATAGTTTAA TTGCATCATG
-3474 AAAATAATCA ATAATACAAT TTATTTGGTT TATTTAAAAA AACTGATTCT TTCTGCTCTC
-3414 TCTATATATA GACTGATTTT ATACTAATGT TGCCTAAAGA TCACCAAATT GTTTGAAGCC
-3354 TAGGTTTCTG AGGGATGGAA AATGATGTCA CAACTATTTA CAGTTCACAC ACACATTCTG
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-3234 TAGAGCTACC ACACCCCAGA GGGTGGTATG GTATGTTGTC TGTTGTGAGC TGTGTGAATC
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-3114 ACTATAATGA CTTTTCAAGA TATAGACAAT ACAGTTAAGA TATAAATGGA AACAAAAAAA
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-2634 CCAGCATTTT GGGAGACTGA GCCGGGTGGA TCACTTGAGC CCAGGAGTTC GAGACCAGCC
-2574 TGGCCAACAT GGCAAAACCC TGTCTCTACT AAAAATACAA AAAATTAGCT GAACATGGTG
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-2454 GAGGTGGAGG TTGCAGTGAG CTAAGATTGA TGGAGCCACT GCACCCCAGC CTAGGTGACA
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-2094 ACCCAATACT GGAGTACTCA GGTATATAAA GCAAATATTA TTAGAGCCAA AGAGAGAGAT
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-1674 ATTAAAGGAT CATTAGAAGA TACTATGAAA CTATATGCTA ATAAATTGGA AAACCTGAAC
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-894 CACCTAAGTT GCTTCCAAAT CTTAGCTATT GTGAATAGTG CTGCAATAAA CATGGGAGTG
-834 TAAATATTTT GTTGACATAC TGATTTCATT TCCTTTGGAT AAATACCCAG TAGTGGGATT
-774 GCTGGATCAT ATGGGGGAAA ATGGAGATGG CTAACGGGCT CAAAAATATA GTTAGAAAAA
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-654 ATATATTATA AAATAACTAA AATAGTATAA ATGGGATGTA TGTAGCAGAG AGAAATGATA

583
-594 AATGTTTGAA GCATTGGATA CTCCATCACC TGCTGTGATA TTATGAATGT CTGCCTATAT
-534 AAATATTCAC TATTCCATAA CACAGCGCCT CTTATGTACC CACAAAAATC
-484 TATTTTCAAA AAAGTTGCTC TAAGAATATA GTTATCAAGT TAAGTAAAAT
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-234 GGAAGGAAAC AATAATGAAA AAAATGTGGT GAGAAAAACA GCTGAAAACC
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-134 GGGGCATTTG GAAAATGTAA ACGAGTATGT TCCCTATTTA AGGCTAGGCA

Cap (-67)
-84 CAAAGCAAGG TCTTCAGAGA ACCTGGAGCC TAAGGTTTAG GCTCACCCAT

ATG (1)
-34 TTCAACCAGT CTAGCAGCAT CTGCAACATC TACAATGGCC TTGACCTTTG

FIG. 6B

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GCTGGATCAT A

FIG. 7B

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FIG 7A

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Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
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130 135 140
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<120> GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY

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Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45

Cap
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ATG (1)
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TTGACCTTTG CTTTACTGGT GGCCCTCCTG GTGCTCAGCT GCAAGTCAAG CTGCTCTGTG

GGC

FIG. 8

INTERNATIONAL SEARCH REPORT

Inte .donal Application No
PCT/US 99/09925

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/67 C12N15/90 C12N15/85 C12N15/21 C07K14/56
A61K48/00 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	C. GEISEL ET AL: "The sequence of Homo sapiens PAC clone DJ0320J15" EMBL DATABASE ENTRY AC004081, ACCESSION NUMBER AC004081, 3 February 1998 (1998-02-03), XP002111521	9,42
A	abstract & UNPUBLISHED,	18,22-24

X	C. STRONG ET AL: "The sequence of H. sapiens BAC clone GS009G13" EMBL DATABASE ENTRY AC002479, ACCESSION NUMBER AC002479 , 26 August 1997 (1997-08-26), XP002111693 & UNPUBLISHED,	9,42

	-/--	

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

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"P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
10 August 1999	20/08/1999

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk	

INTERNATIONAL SEARCH REPORT

Inte .ional Application No
PCT/US 99/09925

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 95 31560 A (HEARTLEIN MICHAEL W ;TRANSKARYOTIC THERAPIES INC (US); TRECO DOUGL) 23 November 1995 (1995-11-23) see the whole document especially page 97, line 1 - page 99, line 13; claims; example 9 figure 11 & US 5 641 670 A cited in the application	1-8, 28-41, 43-46
Y	LAWN R M ET AL: "DNA SEQUENCE OF A MAJOR HUMAN LEUKOCYTE INTERFERON GENE" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 78, no. 9, 1 September 1981 (1981-09-01), pages 5435-5439, XP000605270 The whole document especially page 5437 figure no. 3	1-8, 28-41, 43-46

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 99/09925

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 32 and 44 (as far as they concern an in vivo method) and claims 33-36, 45 are directed to a method of treatment of the human/animal body (Rule 39.1 IV PCT), the search has been carried out and based on the alleged effects of the compound/composition.

2. [X] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
Claims 41-42 and 46 (all partially)
See FURTHER INFORMATION Sheet PCT/ISA/210

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US 99/09925

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 41-42 and 46 all partially

Sequence ID no. 19 in claims 41 and 42 claiming a nucleic acid comprising at least 20 contiguous nucleotides of sequence ID no.19, has not been searched due to the fact that this sequence is 19 nucleotides long.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int. ..tional Application No
PCT/US 99/09925

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9531560 A	23-11-1995	US	5641670 A	24-06-1997
		AU	2550495 A	05-12-1995
		BR	9507874 A	19-08-1997
		CA	2190289 A	23-11-1995
		CN	1119545 A	03-04-1996
		CZ	9603258 A	17-12-1997
		EP	0759082 A	26-02-1997
		FI	964536 A	09-01-1997
		HU	76844 A	28-11-1997
		JP	10500570 T	20-01-1998
		NO	964802 A	09-01-1997
		NZ	285945 A	25-03-1998
		SK	146196 A	04-02-1998
		US	5733746 A	31-03-1998
		ZA	9503879 A	18-01-1996

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NE	Niger
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NO	Norway
NZ	New Zealand
PL	Poland
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RO	Romania
RU	Russian Federation
SD	Sudan
SE	Sweden
SG	Singapore
SI	Slovenia
SK	Slovakia
SN	Senegal
SZ	Swaziland
TD	Chad
TG	Togo
TJ	Tajikistan
TM	Turkmenistan
TR	Turkey
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UZ	Uzbekistan
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ZW	Zimbabwe